



TECH

1600  
1600

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/09/443,986C

DATE: 02/04/2003

TIME: 13:14:34

Input Set : A:\EP.txt

Output Set: N:\CRF4\02042003\I443986C.raw

3 <110> APPLICANT: Elan Corporation  
 4 O'Mahony, Daniel J.  
 6 <120> TITLE OF INVENTION: RETRO-INVERSION PEPTIDES THAT TARGET GIT TRANSPORT RECEPTORS  
 AND RELATED  
 7 METHODS  
 9 <130> FILE REFERENCE: 25,478-A USA  
 11 <140> CURRENT APPLICATION NUMBER: US 09/443,986C  
 12 <141> CURRENT FILING DATE: 1999-11-19  
 14 <160> NUMBER OF SEQ ID NOS: 85  
 16 <170> SOFTWARE: PatentIn version 3.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 15  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: Artificial Sequence  
 23 <220> FEATURE:  
 24 <223> OTHER INFORMATION: PAX2 15 mer fragment-D form retroinversion  
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 29 1 5 10 15  
 32 <210> SEQ ID NO: 2  
 33 <211> LENGTH: 16  
 34 <212> TYPE: PRT  
 35 <213> ORGANISM: Artificial Sequence  
 37 <220> FEATURE:  
 38 <223> OTHER INFORMATION: P31 16 mer fragment- D form retroinversion  
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 43 1 5 10 15  
 46 <210> SEQ ID NO: 3  
 47 <211> LENGTH: 14  
 48 <212> TYPE: PRT  
 49 <213> ORGANISM: Artificial Sequence  
 51 <220> FEATURE:  
 52 <223> OTHER INFORMATION: HAX42 14 mer fragment-D form retroinversion  
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 61 <211> LENGTH: 15  
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 63 <213> ORGANISM: Artificial Sequence  
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 66 <223> OTHER INFORMATION: PAX2 15 mer fragment  
 68 <400> SEQUENCE: 4

16  
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71 1 5 10 15  
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75 <211> LENGTH: 16  
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85 1 5 10 15  
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89 <211> LENGTH: 14  
90 <212> TYPE: PRT  
91 <213> ORGANISM: Artificial Sequence  
93 <220> FEATURE:  
94 <223> OTHER INFORMATION: HAX42 14 mer fragment  
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99 1 5 10  
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103 <211> LENGTH: 40  
104 <212> TYPE: PRT  
105 <213> ORGANISM: Artificial Sequence  
107 <220> FEATURE:  
108 <223> OTHER INFORMATION: PAX2 full length  
110 <400> SEQUENCE: 7  
112 Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
113 1 5 10 15  
116 Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu  
117 20 25 30  
120 Arg Thr Arg Ser Arg Pro Asn Gly  
121 35 40  
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129 <220> FEATURE:  
130 <223> OTHER INFORMATION: HAX42 full length, N-terminal Lysine is dansylated  
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133 <221> NAME/KEY: MOD\_RES  
134 <222> LOCATION: (1)..(1)  
135 <223> OTHER INFORMATION: Dansylated L-Lysine  
138 <400> SEQUENCE: 8  
140 Lys Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys  
141 1 5 10 15  
144 Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg  
145 20 25 30  
148 Lys Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr

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159      tional L-lysine in position 1
161 <220> FEATURE:
162 <221> NAME/KEY: MOD_RES
163 <222> LOCATION: (1)..(1)
164 <223> OTHER INFORMATION: Dansylated L-lysine
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168 Lys Arg Thr Arg Leu Arg Arg Asn His Ser Ser His Lys Ala Asn Thr
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175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: ZElan 145; P31 16 mer fragment- D form retroinversion with
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180      onal L-lysine in position 1
182 <220> FEATURE:
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184 <222> LOCATION: (1)..(1)
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201 <213> ORGANISM: Artificial Sequence
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205      ional L-Lysine in position 1
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209 <222> LOCATION: (1)..(1)
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220 <211> LENGTH: 16
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224 <220> FEATURE:

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Input Set : A:\EP.txt  
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225 <223> OTHER INFORMATION: ZElan 129; PAX2 15 mer fragment with additional L-Lysine in  
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226 tition 1  
228 <220> FEATURE:  
229 <221> NAME/KEY: MOD\_RES  
230 <222> LOCATION: (1)..(1)  
231 <223> OTHER INFORMATION: dansylated L-Lysine  
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237 1 5 10 15  
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243 <213> ORGANISM: Artificial Sequence  
245 <220> FEATURE:  
246 <223> OTHER INFORMATION: ZElan 031; P31 16 mer fragment with additional L-Lysine in  
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249 <220> FEATURE:  
250 <221> NAME/KEY: MOD\_RES  
251 <222> LOCATION: (1)..(1)  
252 <223> OTHER INFORMATION: dansylated L-Lysine  
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258 1 5 10 15  
261 Gly  
265 <210> SEQ ID NO: 14  
266 <211> LENGTH: 15  
267 <212> TYPE: PRT  
268 <213> ORGANISM: Artificial Sequence  
270 <220> FEATURE:  
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272 tition 1  
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275 <221> NAME/KEY: MOD\_RES  
276 <222> LOCATION: (1)..(1)  
277 <223> OTHER INFORMATION: dansylated L-lysine  
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286 <210> SEQ ID NO: 15  
287 <211> LENGTH: 41  
288 <212> TYPE: PRT  
289 <213> ORGANISM: Artificial Sequence  
291 <220> FEATURE:  
292 <223> OTHER INFORMATION: PAX2 full length, N-terminal Lysine is dansylated  
294 <220> FEATURE:  
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296 <222> LOCATION: (1)..(1)  
297 <223> OTHER INFORMATION: dansylated L-Lysine  
300 <400> SEQUENCE: 15

RAW SEQUENCE LISTING  
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Input Set : A:\EP.txt  
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302 Lys Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val  
303 1 5 10 15  
306 Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg  
307 20 25 30  
310 Leu Arg Thr Arg Ser Arg Pro Asn Gly  
311 35 40  
314 <210> SEQ ID NO: 16  
315 <211> LENGTH: 44  
316 <212> TYPE: PRT  
317 <213> ORGANISM: Artificial Sequence  
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320 <223> OTHER INFORMATION: S15 44 mer fragment L-form  
322 <400> SEQUENCE: 16  
324 Arg Ser Gly Ala Tyr Glu Ser Pro Asp Gly Arg Gly Gly Arg Ser Tyr  
325 1 5 10 15  
328 Val Gly Gly Gly Gly Cys Gly Asn Ile Gly Arg Lys His Asn Leu  
329 20 25 30  
332 Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp  
333 35 40  
336 <210> SEQ ID NO: 17  
337 <211> LENGTH: 44  
338 <212> TYPE: PRT  
339 <213> ORGANISM: Artificial Sequence  
341 <220> FEATURE:  
342 <223> OTHER INFORMATION: S21 44 mer fragment L-form  
344 <400> SEQUENCE: 17  
346 Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly  
347 1 5 10 15  
350 Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr  
351 20 25 30  
354 Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser  
355 35 40  
358 <210> SEQ ID NO: 18  
359 <211> LENGTH: 44  
360 <212> TYPE: PRT  
361 <213> ORGANISM: Artificial Sequence  
363 <220> FEATURE:  
364 <223> OTHER INFORMATION: S22 44 mer fragment L-form  
366 <400> SEQUENCE: 18  
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369 1 5 10 15  
372 Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr  
373 20 25 30  
376 Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala  
377 35 40  
380 <210> SEQ ID NO: 19  
381 <211> LENGTH: 44  
382 <212> TYPE: PRT  
383 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:73; Xaa Pos. 1,3,4,6,7,8,10  
Seq#:74; Xaa Pos. 2,4,7,8  
Seq#:75; Xaa Pos. 7,8

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6